

IAP9 Rec'd PCT/PTO 17 MAY 2006

64851-02.ST25

SEQUENCE LISTING

<110> The Government of the United States of America, as
represented by the Secretary of the Department of Health and
Human Services
Flomerfelt, Francis
Gress, Ronald

<120> SPATIAL FOR ALTERING CELL PROLIFERATION

<130> 4239-64851-02

<150> PCT/US2003/036874

<151> 2003-11-18

<160> 7

<170> PatentIn version 3.3

<210> 1

<211> 933

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (84)..(677)

<223> Coding sequence

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Leu Phe Leu Gly Asn Val Tyr Lys Gly Ser
1 5 10

tta gca cct cgt agg gat gag gtg act agt cca aag gca gag ccc cag 161
Leu Ala Pro Arg Arg Asp Glu Val Thr Ser Pro Lys Ala Glu Pro Gln
15 20 25

cca gag acg aag ccg gag aac ctt cca agg agc cac ggg gat gtt ggg 209
Pro Glu Thr Lys Pro Glu Asn Leu Pro Arg Ser His Gly Asp Val Gly
30 35 40

ctc cag aaa gag act gtg gtc cca ggc att gtg gat ttc gag ctg atc 257
Leu Gln Lys Glu Thr Val Val Pro Gly Ile Val Asp Phe Glu Leu Ile
45 50 55

cat gag gag ctg aag acc aca aag ccc caa aca tca caa cca aca ccc 305
His Glu Glu Leu Lys Thr Thr Lys Pro Gln Thr Ser Gln Pro Thr Pro
60 65 70

agt gcc tac cgc ttt gga cgc cta agc cac cat tcc ttc ttc tcg agg 353
Ser Ala Tyr Arg Phe Gly Arg Leu Ser His His Ser Phe Phe Ser Arg
75 80 85 90

cac cac ccc caa cca cag cga gtg act cat atc caa gat atc gct ggg 401
His His Pro Gln Pro Gln Arg Val Thr His Ile Gln Asp Ile Ala Gly

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95

100

105

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Gln Pro Thr Phe Leu Ser Arg Cys Leu Met Gly Met Pro Thr Ile Ser
125 130 135

gtc ccc att ggg gat cca cag tcc aat cgg aac ccc cag ctt tct act 545
Val Pro Ile Gly Asp Pro Gln Ser Asn Arg Asn Pro Gln Leu Ser Thr
140 145 150

tct gac acc tgg agg aag aaa ctg aag gac ctg gct tcc cga gtg act 593
Ser Asp Thr Trp Arg Lys Lys Leu Lys Asp Leu Ala Ser Arg Val Thr
155 160 165 170

gtc ttc act aag gaa atc cag cca aag ccc gat gag gtt ggt gtt gca 641
Val Phe Thr Lys Glu Ile Gln Pro Lys Pro Asp Glu Val Gly Val Ala
175 180 185

caa aga atg gag cct aga aaa aaa agg cct tct taa gtctcccaaa 687
Gln Arg Met Glu Pro Arg Lys Lys Arg Pro Ser
190 195

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tcaaagaaac acaaaatcac acctagcaga gaaatccaag aagggttccc agaaacaccc 807

tctaaagcaa ctgttcccaa cctgtctaat gccttgaccc ttgaatacag tttctcacac 867

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<212> PRT

<213> Mus musculus

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Glu Val Thr Ser Pro Lys Ala Glu Pro Gln Pro Glu Thr Lys Pro Glu
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Asn Leu Pro Arg Ser His Gly Asp Val Gly Leu Gln Lys Glu Thr Val
35 40 45

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Val Pro Gly Ile Val Asp Phe Glu Leu Ile His Glu Glu Leu Lys Thr
50 55 60

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Thr Lys Pro Gln Thr Ser Gln Pro Thr Pro Ser Ala Tyr Arg Phe Gly
65 70 75 80

Arg Leu Ser His His Ser Phe Phe Ser Arg His His Pro Gln Pro Gln
85 90 95

Arg Val Thr His Ile Gln Asp Ile Ala Gly Lys Pro Val Cys Val Val
100 105 110

Arg Asp Glu Phe Ser Leu Ser Ala Leu Thr Gln Pro Thr Phe Leu Ser
115 120 125

Arg Cys Leu Met Gly Met Pro Thr Ile Ser Val Pro Ile Gly Asp Pro
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Gln Ser Asn Arg Asn Pro Gln Leu Ser Thr Ser Asp Thr Trp Arg Lys
145 150 155 160

Lys Leu Lys Asp Leu Ala Ser Arg Val Thr Val Phe Thr Lys Glu Ile
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Lys Lys Arg Pro Ser
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Leu Phe Leu Gly Asn Val Tyr Lys Gly Ser
1 5 10
tta gca cct cgt agg gat gag gtg act agt cca aag gca gag ccc cag 161
Leu Ala Pro Arg Arg Asp Glu Val Thr Ser Pro Lys Ala Glu Pro Gln
15 20 25

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gct ggg aag cct gtc tgc gtg gtc agg gac gag ttc tct ctg tcg gcc Ala Gly Lys Pro Val Cys Val Val Arg Asp Glu Phe Ser Leu Ser Ala 140 145 150	545
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atc tct gtc ccc att ggg gat cca cag tcc aat cgg aac ccc cag ctt Ile Ser Val Pro Ile Gly Asp Pro Gln Ser Asn Arg Asn Pro Gln Leu 175 180 185	641
tct act tct gac acc tgg agg aag aaa ctg aag gac ctg gct tcc cga Ser Thr Ser Asp Thr Trp Arg Lys Lys Leu Lys Asp Leu Ala Ser Arg 190 195 200	689
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1035

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Asn Leu Pro Arg Ser His Gly Asp Val Gly Leu Gln Lys Glu Thr Val
 35 40 45

Val Pro Gly Ile Val Asp Phe Glu Leu Ile His Glu Glu Leu Lys Thr
 50 55 60

Thr Lys Pro Gln Thr Ser Gln Pro Thr Pro Ser Ala Tyr Arg Phe Gly
 65 70 75 80

Arg Leu Ser His His Ser Phe Phe Ser Arg His His Pro Gln Pro Gln
 85 90 95

Arg Val Thr His Ile Gln Val Thr Gly Arg Glu Asp Leu Glu His Ser
 100 105 110

Leu Pro Leu Thr Thr Ser Phe Gln Leu Leu Gln Ala Pro Gly Val Gln
 115 120 125

Pro Met Asp Leu Thr Pro Ser Ala Asp Ile Ala Gly Lys Pro Val Cys
 130 135 140

Val Val Arg Asp Glu Phe Ser Leu Ser Ala Leu Thr Gln Pro Thr Phe
 145 150 155 160

Leu Ser Arg Cys Leu Met Gly Met Pro Thr Ile Ser Val Pro Ile Gly
 165 170 175

Asp Pro Gln Ser Asn Arg Asn Pro Gln Leu Ser Thr Ser Asp Thr Trp
 180 185 190

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Arg Lys Lys Leu Lys Asp Leu Ala Ser Arg Val Thr Val Phe Thr Lys
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Pro Arg Lys Lys Arg Pro Ser
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 Gly Cys Gly Asp Thr Gly Asp Trp Glu Gly Arg Trp Asn His Val Lys
 10 15 20

aag ttc ctc gag cgg tct gga ccc ttc aca cac ccc gat ttc gaa cca 150
 Lys Phe Leu Glu Arg Ser Gly Pro Phe Thr His Pro Asp Phe Glu Pro
 25 30 35

agc act gaa tca ctc cag ttc ttg tta gat aca tgt aaa gtt cta gtc 198
 Ser Thr Glu Ser Leu Gln Phe Leu Leu Asp Thr Cys Lys Val Leu Val
 40 45 50

att gga gct ggt ggc tta gga tgt gag ctt ctg aaa aat ctg gca tta 246
 Ile Gly Ala Gly Gly Leu Gly Cys Glu Leu Leu Lys Asn Leu Ala Leu
 55 60 65

tct ggt ttt aga cag att cat gtt ata gac atg gac act ata gat gtt 294
 Ser Gly Phe Arg Gln Ile His Val Ile Asp Met Asp Thr Ile Asp Val
 70 75 80 85

tcc aat tta aat aga cag ttt tta ttt agg cct aaa gat gty gga aga 342
 Ser Asn Leu Asn Arg Gln Phe Leu Phe Arg Pro Lys Asp Xaa Gly Arg
 90 95 100

ccc aag gct gaa gtt gct gca gaa ttc cta aat gac aga gtt cct aac 390
 Pro Lys Ala Glu Val Ala Ala Glu Phe Leu Asn Asp Arg Val Pro Asn
 105 110 115

tgc aac gtg gtm cca cat ttc aac aag atw caa gat ttt aac gac act 438
 Cys Asn Val Xaa Pro His Phe Asn Lys Xaa Gln Asp Phe Asn Asp Thr
 120 125 130

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gcg aga aga tgg atc aat gga atg ctg ata tct ctt cta aat tat gaa Ala Arg Arg Trp Ile Asn Gly Met Leu Ile Ser Leu Leu Asn Tyr Glu 150 155 160 165	534
gat ggt gtg ttg gat cca agc tcc att gta cct ttg ata gat ggg ggg Asp Gly Val Leu Asp Pro Ser Ser Ile Val Pro Leu Ile Asp Gly Gly 170 175 180	582
aca gaa ggc ttt aaa ggg aat gcc cga gtg att ttg cct gga atg acc Thr Glu Gly Phe Lys Gly Asn Ala Arg Val Ile Leu Pro Gly Met Thr 185 190 195	630
gct tgt att gag tgc act ctg gaa ctt tac cca cca cag gtc aat ttc Ala Cys Ile Glu Cys Thr Leu Glu Leu Tyr Pro Pro Gln Val Asn Phe 200 205 210	678
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agg aca ctt tac tta cag tca gta acg tct att gaa gaa cga acc agg	1254
Arg Thr Leu Tyr Leu Gln Ser Val Thr Ser Ile Glu Glu Arg Thr Arg	
390 395 400 405	
ccc aat ctt tcc aaa aca tta aaa gaa ctg gga cta gtt gat gga caa	1302
Pro Asn Leu Ser Lys Thr Leu Lys Glu Leu Gly Leu Val Asp Gly Gln	
410 415 420	
gaa ctg gct gtt gct gat gtc act aca cca cag act gta cta ttc aaa	1350
Glu Leu Ala Val Ala Asp Val Thr Thr Pro Gln Thr Val Leu Phe Lys	
425 430 435	
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Leu His Phe Thr	
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<223> The 'Xaa' at location 99 stands for Val.

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<222> (121)..(121)

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<222> (127)..(127)

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<222> (222)..(222)

<223> The 'Xaa' at location 222 stands for Pro.

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35 40 45

Cys Lys Val Leu Val Ile Gly Ala Gly Gly Leu Gly Cys Glu Leu Leu
50 55 60

Lys Asn Leu Ala Leu Ser Gly Phe Arg Gln Ile His Val Ile Asp Met
65 70 75 80

Asp Thr Ile Asp Val Ser Asn Leu Asn Arg Gln Phe Leu Phe Arg Pro
85 90 95

Lys Asp Xaa Gly Arg Pro Lys Ala Glu Val Ala Ala Glu Phe Leu Asn
100 105 110

Asp Arg Val Pro Asn Cys Asn Val Xaa Pro His Phe Asn Lys Xaa Gln
115 120 125

Asp Phe Asn Asp Thr Phe Tyr Arg Gln Phe His Ile Ile Val Cys Gly
130 135 140

Leu Asp Ser Ile Ile Ala Arg Arg Trp Ile Asn Gly Met Leu Ile Ser
145 150 155 160

Leu Leu Asn Tyr Glu Asp Gly Val Leu Asp Pro Ser Ser Ile Val Pro
165 170 175

Leu Ile Asp Gly Gly Thr Glu Gly Phe Lys Gly Asn Ala Arg Val Ile

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Leu Pro Gly Met Thr Ala Cys Ile Glu Cys Thr Leu Glu Leu Tyr Pro		
195	200	205
Pro Gln Val Asn Phe Pro Met Cys Thr Ile Ala Ser Met Xaa Arg Leu		
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Pro Glu His Cys Ile Glu Tyr Val Arg Met Leu Gln Trp Pro Lys Glu		
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Gln Pro Phe Gly Asp Gly Val Pro Leu Asp Gly Asp Asp Pro Glu His		
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Ile Arg Gly Val Thr Tyr Arg Leu Thr Gln Gly Val Val Lys Arg Ile		
275	280	285
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Thr Glu Val Phe Lys Ile Ala Thr Ser Ala Tyr Ile Pro Leu Asn Asn		
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Tyr Leu Val Phe Asn Asp Val Asp Gly Leu Tyr Thr Tyr Thr Phe Glu		
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Ala Glu Arg Lys Glu Asn Cys Pro Ala Cys Ser Gln Leu Pro Gln Asn		
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Ile Gln Phe Ser Pro Ser Ala Lys Leu Gln Glu Val Leu Asp Tyr Leu		
355	360	365
Thr Asn Ser Ala Ser Leu Gln Met Lys Ser Pro Ala Ile Thr Ala Thr		
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Leu Glu Gly Lys Asn Arg Thr Leu Tyr Leu Gln Ser Val Thr Ser Ile		
385	390	395
Glu Glu Arg Thr Arg Pro Asn Leu Ser Lys Thr Leu Lys Glu Leu Gly		
405	410	415

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<212> DNA

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